IN THE SPECIFICATION

Please replace Table 2 with the following replacement Table:

Table 2. Gene/polypeptide segments with amino acid sequences.

SEQ ID NO. (amino acid)	SEQ ID NO. (nucleotide)	AviIII Segment	Segment Data
1	2	Total length	SEQ ID NO: 1 (see Table 3 [[1]]); SEQ ID NO: 2 (see Table 4 [[2]])
8		Signal (potential)	MRSRRLVSLLAATASFAVAAALGVLPIAITASPAHA
3		CD (GH74)	ATTQPYTWSNVAIGGGGFVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLD WVGWNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATW QITPLPFKLGGNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMT NFPDVGTYIANPTDTTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFW SRDGGATWQAVPGAPTGFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVT SGTWTRISPVPSTDTANDYFGYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGAT WTRIWDWTSYPNRSLRYVLDISAEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNS DRMLYGTGATLYATNDLTKWDSGGQIHIAPMVKGLEETAVNDLISPPSGAPLISALG DLGGFTHADVTAVPSTIFTSPVFTTGTSVDYAELNPSIIVRAGSFDPSSQPNDRHVAFS TDGGKNWFQGSEPGGVTTGGTVAASADGSRFVWAPGDPGQPVVYAVGFGNSWAA SQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGVTFQPVAAGLPSSGAVGVMFH AVPGKEGDLWLAASSGLYHSTNGGSSWSAITGVSSAVNVGFGKSAPGSSYPAVFVV GTIGGVTGAYRSDDCGTTWVLINDDQHQYGNWGQAITGDHANLRRVYIGTNGRGIV YGDIGGAPSG
4		CBD_III (partial)	VSGGVKVQYKNNDSAPGDNQIKPGLQVVNTGSSSVDLSTVTVRYWFTRDGGSSTLV YNCDWAAIGCGNIRASFGSVNPATPTADTYLQX*
5		CBD_III (partial)	VSGGVKVQYKNNDSAPGDNQIKPGLQVVNTGSSSVDLSTVTVRYWFTRDGGSSTLV YNCDWAAIGCGNIRASFGSVNPATPTADTYLQ

Please replace Table 5 with the following replacement Table:

Table 5. Multiple amino acid sequence alignment of a AviIII catalytic domain and polypeptides with Glycoside Hydrolase Family 74 catalytic domains.

Multialignment of related Glycoside Hydrolase Family 74 catalytic domain
GH74_Ace: *Acidothermus cellulolyticus* AviIII catalytic domain GH74 SEQ ID NO: 3
AviIII_Aac: *Aspergillus aculeatus* Avicelase III (endoglucanase). GeneBank Acc. # BAA29031 SEQ ID NO: 7

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GH74_Ace    ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac  AASQAYTWKNVVTGGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
            *::*.***.**. **** *. ***** .* *: *.****** ** :: :  * **:****

GH74_Ace    WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac  NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG
            :.*   *: ::*:**::*::*:.******* .**** *:****;*** ** * ****:*

GH74_Ace    GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac  GNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSFTWTGTYFQDSSS
            ***************::.****** **:***;*** ****::*.*. .***: :.:.

GH74_Ace    TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII_Aac  T--YTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
            *  * ** *:.**:**.:*.* *.*: ******** ..:.** *.*.**** *.* *

GH74_Ace    GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDTANDYF
AviIII_Aac  GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP---TSLASTYY
            **:******:.* ::.***: :* .*****;.* * *:..:***.** *** *. *. *:

GH74_Ace    GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDWTSYPNRSLRYVLDIS
AviIII_Aac  GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDSGATWSPIWEWNGYPSINYYYSYDIS
            **.**::* * *.*;***: .**** ;******.****: **:*...**. . * ***

GH74_Ace    AEPWLTFGVQPNPPVPSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac  NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV
            **:    ...:     ::*** **;*****;*:: ***** *;*. ;***:*** ::

GH74_Ace    HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSV
AviIII_Aac  TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLDAAPNQAYHTPTYGTTNGI
            : .:. *;** ** ,**;**.*..*;**;** *** *;*: *.*. : :*.; * ..;

GH74_Ace    DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGGVTTGGTVAASADGSR
AviIII_Aac  DYAGNKPSNIVRSGASDDYP-----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT
            ***  ;** ***;*; *   .     ;*;*;; *..*; . .. *  *;** ****.

GH74_Ace    FVWAPGDPGQPVVYAVGFGNSWAASQGVPANAQIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac  VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT
            .:  .. .* * : * : : :* ..:*;.* * **: : ..**. * *;;* *.: ..

GH74_Ace    TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac  SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF
            :* ..: * ** ;*..: * *. **;* ::..**;***; **::: * ;**::. ..

GH74_Ace    GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDQHQYGN-WGQAITGDHAN
AviIII_Aac  GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT
            ****;;. .** .;: . **.*.;* ::*;*.**.* ;*.* .* :*. .:.:.**  .

GH74_Ace    LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac  YGRVFRGHERPGHLLRQSQREPAG
            **: * : * :  : *;*
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